

10 Recv 06 JAN 2003

SEQUENCE LISTING

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<120> Method for detecting the expression of an envelope protein of a human endogenous retrovirus and uses of a gene coding for said protein

<130> 112062

<140> 10/069,883

<141> 2002-05-01

<150> PCT/FR00/02429

<151> 2000-09-01

<150> FR-9911141

<151> 1999-09-01

<150> FR-9911793

<151> 1999-09-15

<160> 64

<170> PatentIn version 3.1

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Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala
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His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met
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Val Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser
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Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser
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210 215 220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225 230 235 240

Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr
245 250 255

Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
260 265 270

Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
275 280 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
290 295 300

Leu Tyr Xaa Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile
 305 310 315 320

Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly
 325 330 335

Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
 340 345 350

Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu
 355 360 365

Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg
 370 375 380

Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
 385 390 395 400

Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
 405 410 415

Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
 420 425 430

Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
 435 440 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Phe
 450 455 460

Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
 465 470 475 480

Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
 485 490 495

Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val
 500 505 510

Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525

Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
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<210> 56

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1614)

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Met Ala Leu Pro Tyr His Ile Phe Leu Phe Thr Val Leu Leu Pro Ser
1          5          10          15

ttc act ctc act gca ccc cct cca tgc cgc tgt atg acc agt agc tcc      96
Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser
          20          25          30

cct tac caa gag ttt cta tgg aga atg cag cgt ccc gga aat att gat      144
Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp
          35          40          45

gcc cca tgc tat agg agt ctt tct aag gga acc ccc acc ttc act gcc      192
Ala Pro Cys Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala
          50          55          60

cac acc cat atg ccc cgc aac tgc tat cac tct gcc act ctt tgc atg      240
His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met
65          70          75          80

cat gca aat act cat tat tgg aca gga aaa atg att aat cct agt tgt      288
His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
          85          90          95

cct gga gga ctt gga gtc act gtc tgt tgg act tac ttc acc caa act      336
Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr
          100          105          110

ggt atg tct gat ggg ggt gga gtt caa gat cag gca aga gaa aaa cat      384
Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His
          115          120          125

gta aaa gaa gta atc tcc caa ctc acc cgg gta cat ggc acc tct agc      432
Val Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser
          130          135          140

ccc tac aaa gga cta gat ctc tca aaa cta cat gaa acc ctc cgt acc      480
Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145          150          155          160

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cat act cgc ctg gta agc cta ttt aat acc acc ctc act ggg ctc cat	528
His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His	
165 170 175	
gag gtc tcg gcc caa aac cct act aac tgt tgg ata tgc ctc ccc ctg	576
Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu	
180 185 190	
aac ttc agg cca tat gtt tca atc cct gta cct gaa caa tgg aac aac	624
Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn	
195 200 205	
ttc agc aca gaa ata aac acc act tcc gtt tta gta gga cct ctt gtt	672
Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val	
210 215 220	
tcc aat ctg gaa ata acc cat acc tca aac ctc acc tgt gta aaa ttt	720
Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe	
225 230 235 240	
agc aat act aca tac aca acc aac tcc caa tgc atc agg tgg gta act	768
Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr	
245 250 255	
cct ccc aca caa ata gtc tgc cta ccc tca gga ata ttt ttt gtc tgt	816
Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys	
260 265 270	
ggt acc tca gcc tat cgt tgt ttg aat ggc tct tca gaa tct atg tgc	864
Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys	
275 280 285	
ttc ctc tca ttc tta gtg ccc cct atg acc atc tac act gaa caa gat	912
Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp	
290 295 300	
tta tac agt tat gtc ata tct aag ccc cgc aac aaa aga gta ccc att	960
Leu Tyr Ser Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile	
305 310 315 320	
ctt cct ttt gtt ata gga gca gga gtg cta ggt gca cta ggt act ggc	1008
Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly	
325 330 335	
att ggc ggt atc aca acc tct act cag ttc tac tac aaa cta tct caa	1056
Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln	
340 345 350	
gaa cta aat ggg gac atg gaa cgg gtc gcc gac tcc ctg gtc acc ttg	1104
Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu	
355 360 365	
caa gat caa ctt aac tcc cta gcg aca gta gtc ctt caa aat cga aga	1152
Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg	
370 375 380	
gct tta gac ttg cta acc gct gaa aga ggg gga acc tgt tta ttt tta	1200
Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu	
385 390 395 400	

ggg gaa gaa tgc tgt tat tat gtt aat caa tcc gga atc gtc act gag 1248
 Gly Glu Glu Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
 405 410 415
 aaa gtt aaa gaa att cga gat cga ata caa cgt aga gca gag gag ctt 1296
 Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
 420 425 430
 cga aac act gga ccc tgg ggc ctc ctc agc caa tgg atg ccc tgg att 1344
 Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
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 ctc ccc ttc tta gga cct cta gca gct ata ata ttg cta ctc ctc ttt 1392
 Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Phe
 450 455 460
 gga ccc tgt atc ttt aac ctc ctt gtt aac ttt gtc tct tcc aga atc 1440
 Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
 465 470 475 480
 gaa gct gta aaa cta caa atg gag ccc aag atg cag tcc aag act aag 1488
 Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
 485 490 495
 atc tac cgc aga ccc ctg gac cgg aat gct agc cca cga tct gat gtt 1536
 Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val
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 aat gac atc aaa ggc acc cct cct gag gaa atc tca gct gca caa cct 1584
 Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525
 cta cta cgc ccc aat tca gca gga agc agt tag 1617
 Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
 530 535

<210> 57

<211> 538

<212> PRT

<213> Homo sapiens

<400> 57

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Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser
 20 25 30

Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp
 35 40 45

Ala Pro Cys Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala
50 55 60

His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met
65 70 75 80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
85 90 95

Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr
100 105 110

Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His
115 120 125

Val Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser
130 135 140

Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145 150 155 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His
165 170 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu
180 185 190

Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
195 200 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
210 215 220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225 230 235 240

Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr
245 250 255

Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
260 265 270

Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
275 280 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
 290 295 300

Leu Tyr Ser Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile
 305 310 315 320

Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly
 325 330 335

Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
 340 345 350

Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu
 355 360 365

Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg
 370 375 380

Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
 385 390 395 400

Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
 405 410 415

Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
 420 425 430

Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
 435 440 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Leu Phe
 450 455 460

Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
 465 470 475 480

Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
 485 490 495

Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val
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Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
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Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
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<210> 58

<211> 1617

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1614)

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ttc act ctc act gca ccc cct cca tgc cgc tgt atg acc agt agc tcc	96
Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser	
20 25 30	
cct tac caa gag ttt cta tgg aga atg cag cgt ccc gga aat att gat	144
Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp	
35 40 45	
gcc cca tgc tat agg agt ctt tct aag gga acc ccc acc ttc act gcc	192
Ala Pro Cys Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala	
50 55 60	
cac acc cat atg ccc cgc aac tgc tat cac tct gcc act ctt tgc atg	240
His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met	
65 70 75 80	
cat gca aat act cat tat tgg aca gga aaa atg att aat cct agt tgt	288
His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys	
85 90 95	
cct gga gga ctt gga gtc act gtc tgt tgg act tac ttc acc caa act	336
Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr	
100 105 110	
ggt atg tct gat ggg ggt gga gtt caa gat cag gca aga gaa aaa cat	384
Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His	
115 120 125	
gta aaa gaa gta atc tcc caa ctc acc cgg gta cat ggc acc tct agc	432
Val Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser	
130 135 140	

ccc tac aaa gga cta gat ctc tca aaa cta cat gaa acc ctc cgt acc	480
Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr	
145 150 155 160	
cat act cgc ctg gta agc cta ttt aat acc acc ctc act ggg ctc cat	528
His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His	
165 170 175	
gag gtc tcg gcc caa aac cct act aac tgt tgg ata tgc ctc ccc ctg	576
Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu	
180 185 190	
aac ttc agg cca tat gtt tca atc cct gta cct gaa caa tgg aac aac	624
Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn	
195 200 205	
ttc agc aca gaa ata aac acc act tcc gtt tta gta gga cct ctt gct	672
Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Ala	
210 215 220	
tcc aat ctg gaa ata acc cat acc tca aac ctc acc tgt gta aaa ttt	720
Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe	
225 230 235 240	
agc aat act aca tac aca acc aac tcc caa tgc atc agg tgg gta act	768
Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr	
245 250 255	
cct ccc aca caa ata gtc tgc cta ccc tca gga ata ttt ttt gtc tgt	816
Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys	
260 265 270	
ggt acc tca gcc tat cgt tgt ttg aat ggc tct tca gaa tct atg tgc	864
Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys	
275 280 285	
ttc ctc tca ttc tta gtg ccc cct atg acc atc tac act gaa caa gat	912
Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp	
290 295 300	
tta tac aat tat gtc ata tct aag ccc cgc aac aaa aga gta ccc att	960
Leu Tyr Asn Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile	
305 310 315 320	
ctt cct ttt gtt ata gga gca gga gtg cta ggt gca cta ggt act ggc	1008
Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly	
325 330 335	
att ggc ggt atc aca acc tct act cag ttc tac tac aaa cta tct caa	1056
Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln	
340 345 350	
gaa cta aat ggg gac atg gaa cgg gtc gcc gac tcc ctg gtc acc ttg	1104
Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu	
355 360 365	
caa gat caa ctt aac tcc cta gcg aca gta gtc ctt caa aat cga aga	1152
Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg	
370 375 380	

gct tta gac ttg cta acc gct gaa aga ggg gga acc tgt tta ttt tta 1200
 Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
 385 390 395 400
 ggg gaa gaa tgc tgt tat tat gtt aat caa tcc gga atc gtc act gag 1248
 Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
 405 410 415
 aaa gtt aaa gaa att cga gat cga ata caa cgt aga gca gag gag ctt 1296
 Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
 420 425 430
 cga aac act gga ccc tgg ggc ctc ctc agc caa tgg atg ccc tgg att 1344
 Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
 435 440 445
 ctc ccc ttc tta gga cct cta gca gct ata ata ttg cta ctc ctc ttt 1392
 Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Leu Phe
 450 455 460
 gga ccc tgt atc ttt aac ctc ctt gtt aac ttt gtc tct tcc aga atc 1440
 Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
 465 470 475 480
 gaa gct gta aaa cta caa atg gag ccc aag atg cag tcc aag act aag 1488
 Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
 485 490 495
 atc tac cgc aga ccc ctg gac cgg aat gct agc cca cga tct gat gtt 1536
 Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val
 500 505 510
 aat gac atc aaa ggc acc cct cct gag gaa atc tca gct gca caa cct 1584
 Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525
 cta cta cgc ccc aat tca gca gga agc agt tag 1617
 Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
 530 535

<210> 59

<211> 538

<212> PRT

<213> Homo sapiens

<400> 59

Met Ala Leu Pro Tyr His Ile Phe Leu Phe Thr Val Leu Leu Pro Ser
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Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser
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Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp
 35 40 45

Ala Pro Cys Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala
 50 55 60

His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met
 65 70 75 80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
 85 90 95

Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr
 100 105 110

Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His
 115 120 125

Val Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser
 130 135 140

Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr
 145 150 155 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His
 165 170 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu
 180 185 190

Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
 195 200 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Ala
 210 215 220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
 225 230 235 240

Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr
 245 250 255

Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
 260 265 270

Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
 275 280 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
 290 295 300

Leu Tyr Asn Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile
 305 310 315 320

Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly
 325 330 335

Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
 340 345 350

Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu
 355 360 365

Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg
 370 375 380

Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
 385 390 395 400

Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
 405 410 415

Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
 420 425 430

Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
 435 440 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Phe
 450 455 460

Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
 465 470 475 480

Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
 485 490 495

Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val
 500 505 510

Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525

Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
 530 535

<210> 60

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1614)

<223>

<400> 60

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 Met Ala Leu Pro Tyr His Ile Phe Leu Phe Thr Val Leu Leu Pro Ser
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ttc act ctc act gca ccc cct cca tgc cgc tgt atg acc agt agc tcc 96
 Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser
 20 25 30

cct tac caa gag ttt cta tgg aga atg cag cgt ccc gga aat att gat 144
 Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp
 35 40 45

gcc cca tgc tat agg agt ctt tct aag gga acc ccc acc ttc act gcc 192
 Ala Pro Cys Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala
 50 55 60

cac acc cat atg ccc cgc aac tgc tat cac tct gcc act ctt tgc atg 240
 His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met
 65 70 75 80

cat gca aat act cat tat tgg aca gga aaa atg att aat cct agt tgt 288
 His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
 85 90 95

cct gga gga ctt gga gtc act gtc tgt tgg act tac ttc acc caa act 336
 Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr
 100 105 110

ggg atg tct gat ggg ggt gga gtt caa gat cag gca aga gaa aaa cat 384
 Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His
 115 120 125

gca	aaa	gaa	gta	atc	tcc	caa	ctc	acc	cgg	gta	cat	ggc	acc	tct	agc	432
Ala	Lys	Glu	Val	Ile	Ser	Gln	Leu	Thr	Arg	Val	His	Gly	Thr	Ser	Ser	
130						135					140					
ccc	tac	aaa	gga	cta	gat	ctc	tca	aaa	cta	cat	gaa	acc	ctc	cgt	acc	480
Pro	Tyr	Lys	Gly	Leu	Asp	Leu	Ser	Lys	Leu	His	Glu	Thr	Leu	Arg	Thr	
145					150					155					160	
cat	act	cgc	ctg	gta	agc	cta	ttt	aat	acc	acc	ctc	act	ggg	ctc	cat	528
His	Thr	Arg	Leu	Val	Ser	Leu	Phe	Asn	Thr	Thr	Leu	Thr	Gly	Leu	His	
				165					170					175		
gag	gtc	tcg	gcc	caa	aac	cct	act	aac	tgt	tgg	ata	tgc	ctc	ccc	ctg	576
Glu	Val	Ser	Ala	Gln	Asn	Pro	Thr	Asn	Cys	Trp	Ile	Cys	Leu	Pro	Leu	
			180					185						190		
aac	ttc	agg	cca	tat	gtt	tca	atc	cct	gta	cct	gaa	caa	tgg	aac	aac	624
Asn	Phe	Arg	Pro	Tyr	Val	Ser	Ile	Pro	Val	Pro	Glu	Gln	Trp	Asn	Asn	
		195					200					205				
ttc	agc	aca	gaa	ata	aac	acc	act	tcc	gtt	tta	gta	gga	cct	ctt	gtt	672
Phe	Ser	Thr	Glu	Ile	Asn	Thr	Thr	Ser	Val	Leu	Val	Gly	Pro	Leu	Val	
	210					215					220					
tcc	aat	ctg	gaa	ata	acc	cat	acc	tca	aac	ctc	acc	tgt	gta	aaa	ttt	720
Ser	Asn	Leu	Glu	Ile	Thr	His	Thr	Ser	Asn	Leu	Thr	Cys	Val	Lys	Phe	
225					230					235					240	
agc	aat	act	aca	tac	aca	acc	aac	tcc	caa	tgc	atc	agg	tgg	gta	act	768
Ser	Asn	Thr	Thr	Tyr	Thr	Thr	Asn	Ser	Gln	Cys	Ile	Arg	Trp	Val	Thr	
				245					250					255		
cct	ccc	aca	caa	ata	gtc	tgc	cta	ccc	tca	gga	ata	ttt	ttt	gtc	tgt	816
Pro	Pro	Thr	Gln	Ile	Val	Cys	Leu	Pro	Ser	Gly	Ile	Phe	Phe	Val	Cys	
			260					265					270			
ggc	acc	tca	gcc	tat	cgt	tgt	ttg	aat	ggc	tct	tca	gaa	tct	atg	tgc	864
Gly	Thr	Ser	Ala	Tyr	Arg	Cys	Leu	Asn	Gly	Ser	Ser	Glu	Ser	Met	Cys	
		275				280						285				
ttc	ctc	tca	ttc	tta	gtg	ccc	cct	atg	acc	atc	tac	act	gaa	caa	gat	912
Phe	Leu	Ser	Phe	Leu	Val	Pro	Pro	Met	Thr	Ile	Tyr	Thr	Glu	Gln	Asp	
	290					295					300					
tta	tac	agt	tat	gtc	ata	tct	aag	ccc	cgc	aac	aaa	aga	gta	ccc	att	960
Leu	Tyr	Ser	Tyr	Val	Ile	Ser	Lys	Pro	Arg	Asn	Lys	Arg	Val	Pro	Ile	
305					310					315					320	
ctt	cct	ttt	gtt	ata	gga	gca	gga	gtg	cta	ggc	gca	cta	ggc	act	ggc	1008
Leu	Pro	Phe	Val	Ile	Gly	Ala	Gly	Val	Leu	Gly	Ala	Leu	Gly	Thr	Gly	
				325					330					335		
att	ggc	ggc	atc	aca	acc	tct	act	cag	ttc	tac	tac	aaa	cta	tct	caa	1056
Ile	Gly	Gly	Ile	Thr	Thr	Ser	Thr	Gln	Phe	Tyr	Tyr	Lys	Leu	Ser	Gln	
			340					345					350			
gaa	cta	aat	ggg	gac	atg	gaa	cgg	gtc	gcc	gac	tcc	ctg	gtc	acc	ttg	1104
Glu	Leu	Asn	Gly	Asp	Met	Glu	Arg	Val	Ala	Asp	Ser	Leu	Val	Thr	Leu	
		355					360						365			

caa gat caa ctt aac tcc cta gcg aca gta gtc ctt caa aat cga aga 1152
 Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg
 370 375 380

 gct tta gac ttg cta acc gct gaa aga ggg gga acc tgt tta ttt tta 1200
 Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
 385 390 395 400

 ggg gaa gaa tgc tgt tat tat gtt aat caa tcc gga atc gtc act gag 1248
 Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
 405 410 415

 aaa gtt aaa gaa att cga gat cga ata caa cgt aga gca gag gag ctt 1296
 Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
 420 425 430

 cga aac act gga ccc tgg ggc ctc ctc agc caa tgg atg ccc tgg att 1344
 Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
 435 440 445

 ctc ccc ttc tta gga cct cta gca gct ata ata ttg cta ctc ctc ttt 1392
 Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Phe
 450 455 460

 gga ccc tgt atc ttt aac ctc ctt gtt aac ttt gtc tct tcc aga atc 1440
 Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
 465 470 475 480

 gaa gct gta aaa cta caa atg gag ccc aag atg cag tcc aag act aag 1488
 Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
 485 490 495

 atc tac cgc aga ccc ctg gac cgg aat gct agc cca cga tct gat gtt 1536
 Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val
 500 505 510

 aat gac atc aaa ggc acc cct cct gag gaa atc tca gct gca caa cct 1584
 Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525

 cta cta cgc ccc aat tca gca gga agc agt tag 1617
 Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
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<211> 538

<212> PRT

<213> Homo sapiens

<400> 61

Met Ala Leu Pro Tyr His Ile Phe Leu Phe Thr Val Leu Leu Pro Ser
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Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser
20 25 30

Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp
35 40 45

Ala Pro Cys Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala
50 55 60

His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met
65 70 75 80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
85 90 95

Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr
100 105 110

Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His
115 120 125

Ala Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser
130 135 140

Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145 150 155 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His
165 170 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu
180 185 190

Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
195 200 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
210 215 220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225 230 235 240

Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr
245 250 255

Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
260 265 270

Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
275 280 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
290 295 300

Leu Tyr Ser Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile
305 310 315 320

Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly
325 330 335

Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
340 345 350

Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu
355 360 365

Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg
370 375 380

Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
385 390 395 400

Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
405 410 415

Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
420 425 430

Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
435 440 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Leu Phe
450 455 460

Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
465 470 475 480

Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
485 490 495

Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val
 500 505 510

Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525

Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
 530 535

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<211> 246

<212> DNA

<213> Homo sapiens

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 gagagctcac taaaatgcta attaggcaaa gacrggaggt aaagaaatag ccaatcatct 180
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<210> 63

<211> 246

<212> DNA

<213> Homo sapiens

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 ggcaac 246

<210> 64

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<212> DNA

<213> Homo sapiens

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gagagctcac taaaatgcta attaggcaaa gacgggaggt aaagaaatag ccaatcatct 180
attgcctgag agcacagcag gagggacaac aatcgggata taaaccagg cattcgagct 240
ggcaac 246

